

Fig. 1

204010 953400

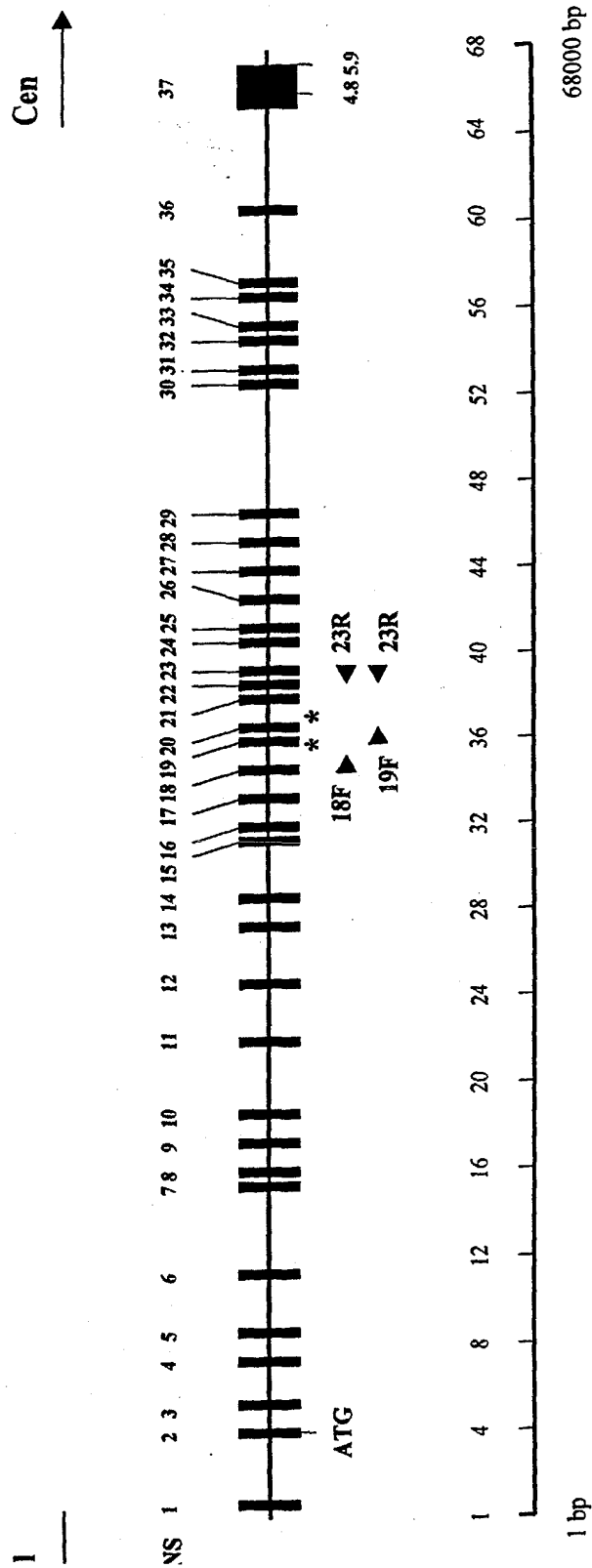


Fig. 2a

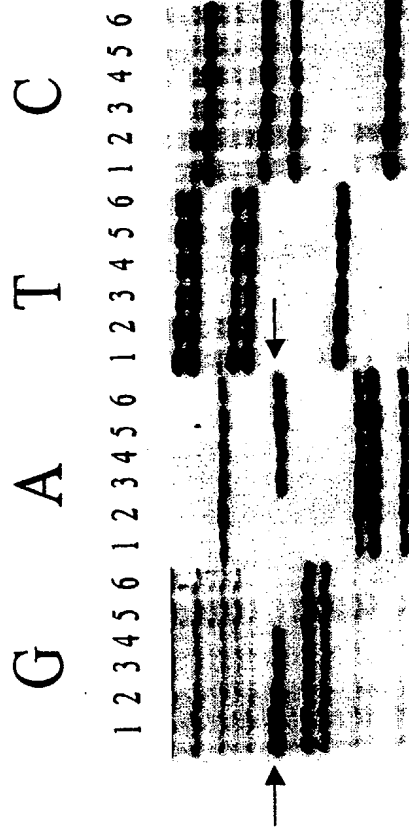


Fig. 2b

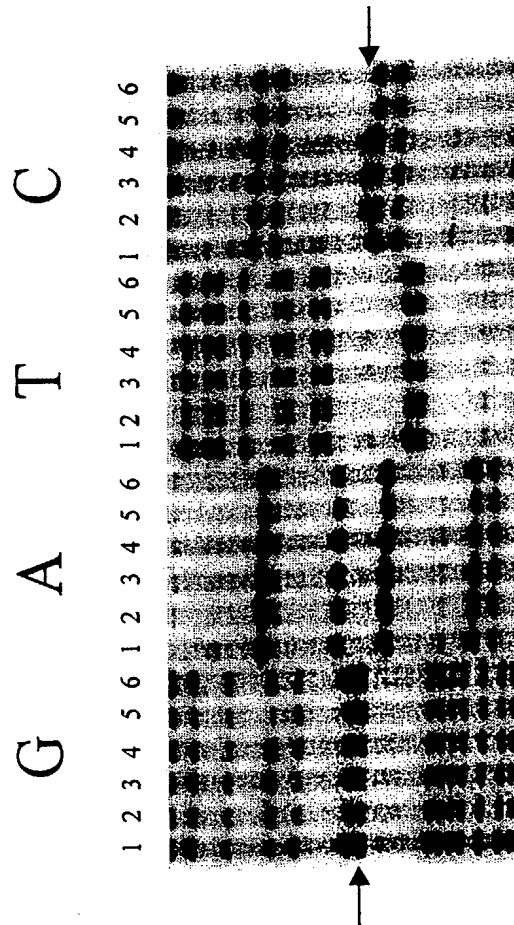


Fig. 2c

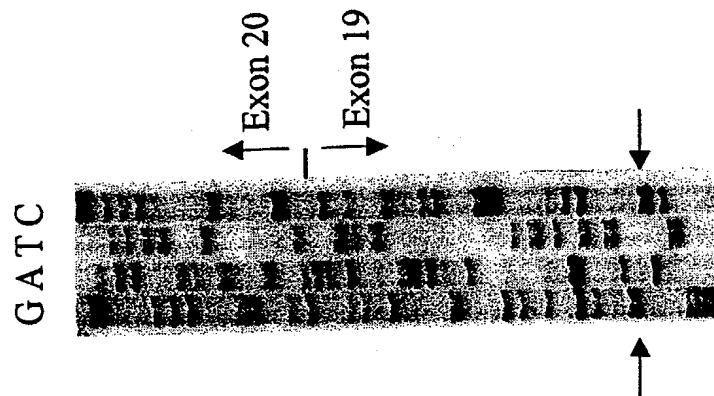


Fig. 3A

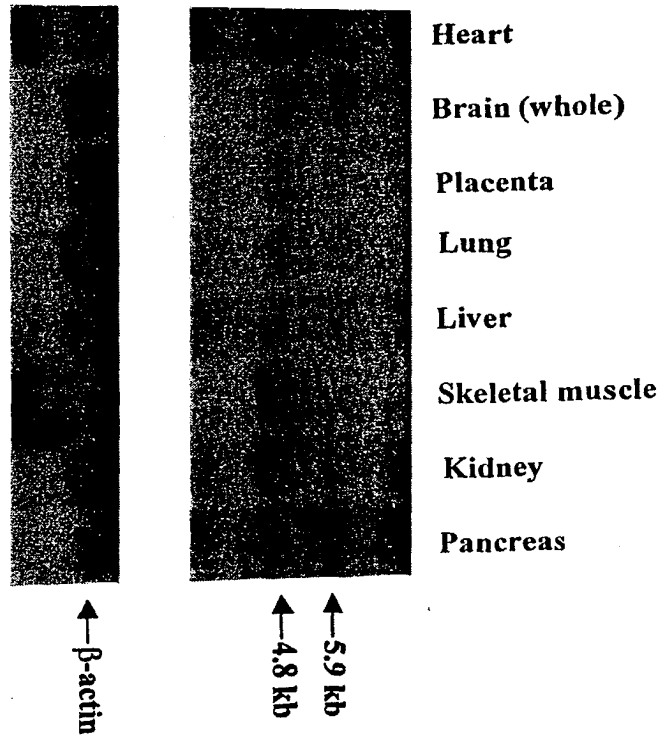
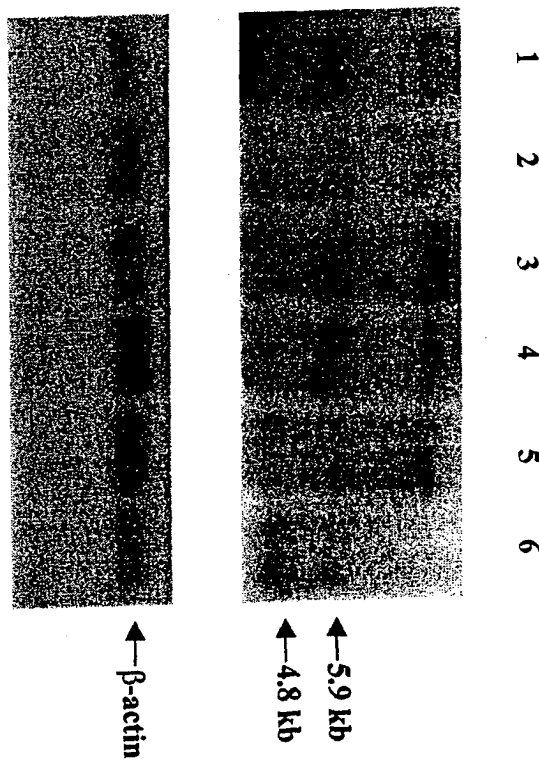


Fig. 3B



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FIG. 4A

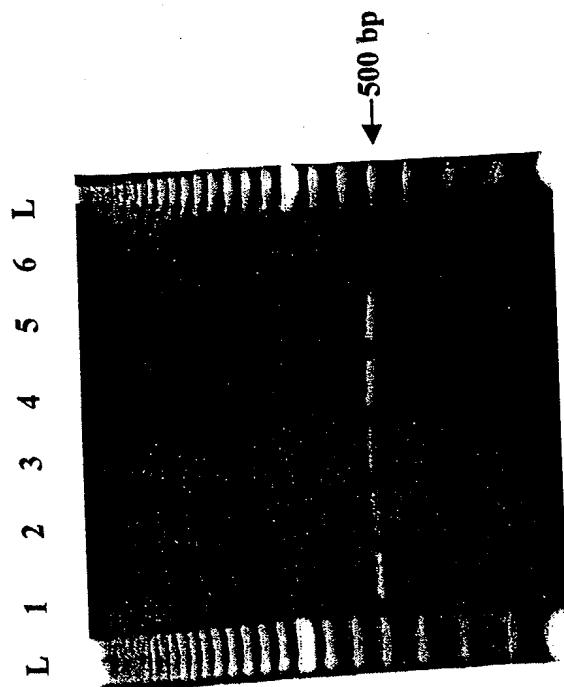
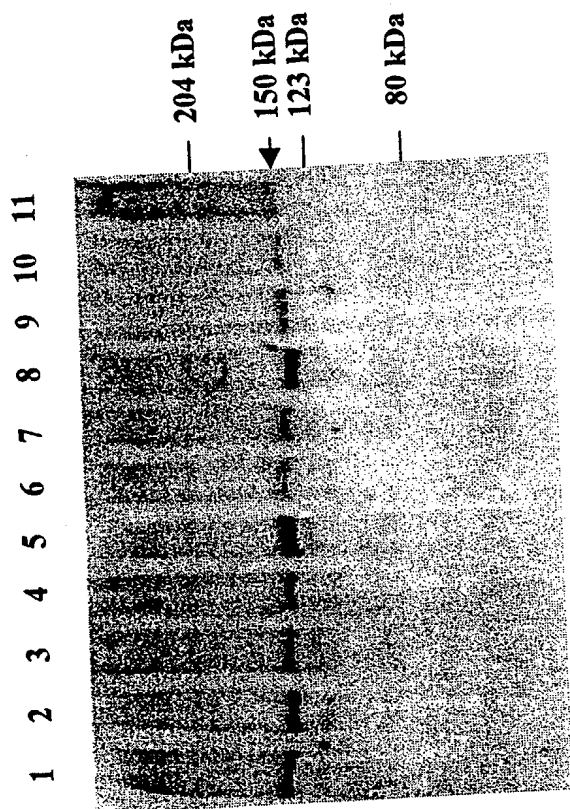


FIG. 4B



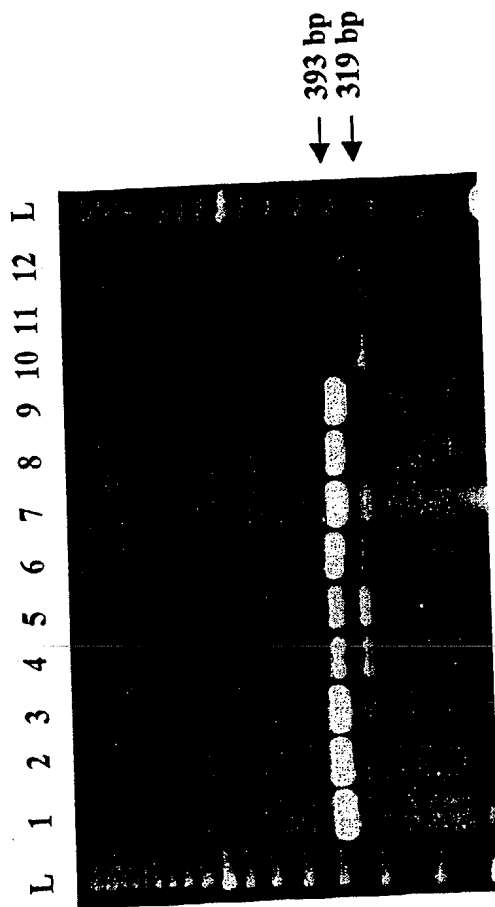


FIG. 5

## FIGURE 6

IKBKAPgenomic.seq Length: 66479

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FIGURE 7

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 61 cagcggttttc ccctggaggg cgccctccatc cttggaggcc tagtgccgtc ggagagagag  
 121 cgggagccgc ggacagagac gcgtgcgcaa ttcggagccg actctgggtg cggactgtgg  
 181 gagctgactc tgggtagccg gctgcgcgtg gctggggagg cgaggccgga cgcacctctg  
 241 tttgggggtc ctccagagatt aatgattcat caagggatag ttgtactgtt ctcggtggaa  
 301 tcaattcacc atgcgaaatc tgaattattt tcggaccctg gagttcaggg atattcaagg  
 361 tccagggaat cctcagtgct tctctctccg aactgaacag gggacgggtc tcattgggtc  
 421 agaacatggc ctgatagaag tagaccctgt ctcaagagaa gtgaaaaatg aagtttcttt  
 481 ggtggcagaa ggctttctcc cagaggatgg aagtggccgc attgttggtg ttcaggactt  
 541 gctggatcag gagtctgtgt gtgtggccac agcctctgga gacgtcatac tctgcagtct  
 601 cagcacacaa cagctggagt gtgtgggag tgtagccagt ggtatctctg ttatgagttg  
 661 gagtcctgac caagagctgg tgcttcttgc cacaggtcaa cagaccctga ttatgatgac  
 721 aaaagatttt gagccaatcc tggagcagca gatccatcag gatgattttg gtgaaagcaa  
 781 gtttatcact gttggatggg gtaggaagga gacacagttc catggatcag aaggcagaca  
 841 agcagctttt cagatgcaaa tgcattgagtc tgctttgccc tgggatgacc atagaccaca  
 901 agttacctgg cggggggatg gacagttttt tgctgtgagt gttgtttgcc cagaaacagg  
 961 ggctcggaag gtcagagtgt ggaaccgaga gtttgctttg cagtcaacca gtgagcctgt  
 1021 ggcaggactg ggaccagccc tggcttgga accctcaggc agtttgattg catctacaca  
 1081 agataaacc caccagcagg atattgtgtt ttttgagaaa aatggactcc ttcattggaca  
 1141 ctttacactt ccttccctta aagatgaggt taaggtaaat gacttgctct ggaatgcaga  
 1201 ttcctctgtg cttgcagtct ggctggaaga ccttcagaga gaagaaagct ccattccgaa  
 1261 aacctgtgtt cagctctgga ctgttgaaaa ctatcactgg tatctcaagc aaagttttatc  
 1321 cttcagcacc tgtgggaaga gcaagattgt gtctctgatg tgggaccctg tgaccccata  
 1381 ccggctgcat gttctctgtc agggctggca ttacctcgcc tatgattggc actggacgac  
 1441 tgaccggagc gtgggagata attcaagtga cttgtccaat gtggctgtca ttgatggaaa  
 1501 cagggtgttg gtgacagtct tccggcagac tgtggttccg cctcccatgt gcacctacca  
 1561 actgctgttc ccacaccctg tgaatcaagt cacattctta gcacaccctc aaaagagtaa  
 1621 tgacctgtct gttctagatg ccagtaacca gatttctgtt tataaatgtg gtgattgtcc  
 1681 aagtgcctgac cctacagtga aactgggagc tgtgggtgga agtggattta aagtttgect  
 1741 tagaactcct catttggaag agagatacaa aatccagttt gagaataatg aagatcaaga  
 1801 tgtaaaccgc ctgaaactag gccttctcac ttggattgaa gaagacgtct tccctggctgt  
 1861 aagccacagt gagttcagcc cccggtctgt cattcaccat ttgactgcag cttctctctga  
 1921 gatggatgaa gagcatggac agctcaatgt cagttcatct gcagcgggtg atggggctcat  
 1981 aatcagctca tgttgcaatt ccaagaccaa gtcagtagta ttacagctgg ctgatggcca  
 2041 gatatttaag tacctttggg agtcaccttc tctggctatt aaacctgga agaactctgg  
 2101 tggatttctt gttcggtttc cttatccatg caccagacc gaattggcca tgattggaga  
 2161 agaggaatgt gtccttggtc tgactgacag gtgtcgcttt ttcataaatg acattgaggt  
 2221 tgcgtcaaat atcacgtcat ttgcagtata tgatgagttt ttattgttga caaccattc  
 2281 ccatacctgc cagtgttttt gcctgaggga tgcctcattt aaaacattac aggcgggect  
 2341 gagcagcaat catgtgtccc atggggaagt tctgcggaaa gtggagaggg gttcacggat  
 2401 tgtcactgtt gtgccccagg acacaaagct tgtattacag atgccaaggg gaaacttaga  
 2461 agttgttcat catcgagccc tggtttttagc tcagattcgg aagtgggttg acaaacttat  
 2521 gtttaagag gcatttgaat gcatgagaaa gctgagaatc aatctcaatc tgatttatga  
 2581 tcataaccct aaggtgtttc ttggaaatgt ggaaaccttc attaaacaga tagattctgt  
 2641 gaatcatatt aacttgtttt ttacagaatt gaaagaagaa gatgtcacga agaccatgta  
 2701 ccctgcacca gttaccagca gtgtctacct gtccagggat cctgacggga ataaaataga  
 2761 ccttgctctgc gatgctatga gagcagtcac ggagagcata aatcctcata aatactgctt  
 2821 atccatactt acatctcatg taaagaagac aacccagaaa ctggaaattg tactgcaaaa  
 2881 agtacacgag cttcaaggaa atgctccctc tgatcctgat gctgtgagtg ctgaagaggc  
 2941 cttgaaatat ttgctgcatc tggtagatgt taatgaatta tatgatcatt ctcttggcac  
 3001 ctatgacttt gatttgggtc tcatggtagc tgagaagtca cagaaggatc ccaaagaata  
 3061 tcttccattt cttataacac ttaagaaaat ggaaactaat tatcagcggg ttactataga  
 3121 caaatacttg aaacgatatg aaaaagccat tggccacctc agcaaatgtg gacctgagta

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# Figure 7

Continued

3181	cttcccagaa	tgtttaaaact	tgataaaaaga	taaaaaacttg	tataacgaag	ctctgaagtt
3241	atattccacca	agctcacaaac	agtaccagga	tatcagcatt	gcttatgggg	agcacctgat
3301	gcaggagcac	atgtatgagc	cagcggggct	catgtttgcc	cgttgcgggtg	cccacgagaa
3361	agctctctca	gcctttctca	catgtggcaa	ctggaagcaa	gcccctctgtg	tggcagccca
3421	gcttaactttt	accaaagacc	agctgggtggg	cctcggcaga	actctggcag	gaaagctggt
3481	tgagcagagg	aagcacattg	atgcggccat	ggtttttgaa	gagagtggcc	aggattatga
3541	agaagctgtg	ctcttgctgt	tagaaggagc	tgcttgggaa	gaagctttga	ggctggtata
3601	caaatataac	agactggata	ttatagaaac	caacgtaaaag	ccttccattt	tagaagccca
3661	gaaaaattat	atggcatttc	tggactctca	gacagccaca	ttcagtcgcc	acaagaaacg
3721	tttatttgga	gttcgagagc	tcaaggagca	agcccagcag	gcaggtctgg	atgatgaggt
3781	accccacggg	caagagtcag	acctcttctc	tgaaactagc	agtgtcgtga	gtggcagtga
3841	gatgagtggc	aaatactccc	atagtaactc	caggatatca	gcgagatcat	ccaagaatcg
3901	ccgaaaagcg	gagcgggaaga	agcacagcct	caaagaaggc	agtccgctgg	aggacctggc
3961	cctcctggag	gcactgagtg	aagtgggtgca	gaacactgaa	aacctgaaag	atgaagtata
4021	ccatattttta	aaggtactct	ttctctttga	gtttgatgaa	caaggaaggg	aattacagaa
4081	ggcctttgaa	gatacgtctg	agttgatgga	aaggtcactt	ccagaaattt	ggactcttac
4141	ttaccagcag	aattcagcta	ccccggttct	aggtcccaat	tctactgcaa	atagtatcat
4201	ggcatcttat	cagcaacaga	agacttcggg	tcctgttctt	gatgctgagc	tttttatacc
4261	accaaagatc	aacagaagaa	cccagtggaa	gctgagcctg	ctagactgag	tgactgcagt
4321	taggagggat	ccgacagaga	agaccatttc	cactcattcc	tggtgtccta	ccaccccttg
4381	ctctttgagg	gctggctatt	gagaactgga	aagagtataaa	tgataactta	ccttagcatt
4441	gccaaagaact	tcagcagaca	acaagcaatt	ctattttattt	tatgttgtgt	atacatcttg
4501	atcattagca	agacattaag	ctttaacat	tatggcacca	ttttgtgaga	atgattgttc
4561	tttcacttgg	gctgtttgag	agcataatta	tggtaatcat	gagattaatg	tttcatgatt
4621	tctacctcca	aagtgtgaag	acaagtaaaa	caatgtttct	aaattgtctt	attttgttgg
4681	cggagaagat	tacaatggct	attagtgcct	catttggtca	aatgtaatca	cttaaatagc
4741	ttcttgtcac	cttaaaactaa	agcagaataa	aaagtatcct	ttgaaattat	aagccctcct
4801	ttgctgacag	ctattatttt	gtaacatctt	accaggtcat	gtgctttcag	ttataactgg
4861	gctgagcctc	ctataattac	aatgtctata	gggactgttt	tactgcctgt	gtattttctg
4921	ctagagagtt	agcaatgtta	gagctagaac	agattagaat	ttctaaacag	tatcatgcac
4981	agttgggtgtg	agtgatcagt	gtgcattgta	tggcatgcat	ggttgtgaat	tattctctgt
5041	tctccaaata	ctgtttcttt	aactcagata	tttttgtag	tgtctaggcc	acttcattta
5101	tttttcgtca	tggtacttta	ctgacttctc	tttattcaat	tctccacgcc	ctcaccacaa
5161	aaaactgtct	caaaatgaga	atatttttat	tcttcatggt	gagtctagaa	aacgccccac
5221	ttcattctga	ttaaaaaatt	cttccatggt	tttaaatatc	agaaccagac	ctttcttact
5281	gtgtatctta	gcccatttgt	gtctctataa	caacaaccag	ctttcaaagg	aactaataga
5341	gtgaaaactc	actcattacc	acgaggatgg	cacaagcgat	tcacgtagga	tctgcccttg
5401	tgacccaaac	acctcccatt	gggcccact	tccaacactg	gtgatcacat	ttcaacatga
5461	ggtttaggga	aacaaaatgcc	taaactacag	cactgtacat	aaactaacag	gaaatgctgc
5521	ttttgatcct	caaagaagtg	atatagccaa	aattgtaatt	taagaagcct	ttgtcagtat
5581	agcaagatgt	taactataga	atcaatctag	gagtattcac	tgtaaaattc	aacttttctg
5641	tatgtttgaa	catttttcaca	atctcatagg	agttttttaa	agaagagaa	agaagatata
5701	ctttgctttg	gagaaatcta	ctttttgact	tacatgggtt	tgctgtaatt	aagtgcccaa
5761	tattgaaagg	ctgcaagtac	tttgtaatca	ctctttggca	tgggtaaata	agcatggtaa
5821	cttatattga	aatatagctg	tcttgctttg	gataactgta	aagggaccca	tgctgataga
5881	ctggaaatag	aagtaaatgt	gtttattgaa	aaaaaaaaaa	aaaa	

# FIGURE 8

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1 mrnlklfrtl efrdiqggpn pqcfslrteq gtvligsehg lievdpsvre vknevsllvae
61 gflpedgsgr ivgvqdllldq esvcvatasg dvlcslstq qlecvgsvas gisvmswspd
121 qelvllatgq qtlimntkdf epileqqihq ddfgeskfit vgwgrketqf hgsegrqaaf
181 qmqmhesalp wddhrpqvtw rgdgqffavs vvcpetgark vrvwnrefal qstsepvagl
241 gpalawkpsg sliastqdkp nqqdivffek ngllhghftl pflkdevkvn dllwnadssv
301 lavrledlqr ekssipktcv qlwtvgnyhw ylkqslsfst cgkskivslm wdpvtpyrh
361 vlcqgwhyla ydwhwttdrs vgdnssdlsn vavidgnrvl vtvfrqtvvp ppmctyqlf
421 phpvnqvtfl ahpqksndla vldasnqisv ykcgdcpsad ptvklgavgg sgfkvclrtf
481 hlekrykiqf ennedqdvnp lklglitwie edvflavshs efsprsvihh ltaassemde
541 ehgqlnvsss aavdgviisl ccnsktksv lqladggqfk ylwespslai kpwnsggfp
601 vrfpypctqt elamigeeec vlgltldrcrf findievasn itsfavydef llltthshc
661 qcfcldasf ktlqaglssn hvshgevlrk vergsrivtv vpgdtklvlq mprgnlevvh
721 hralvlaqir kwldklmfke afecmrklri nlnpiydhnp kvflgnvetf ikqidsvnhi
781 nlfftelkee dvtktmypap vtssvylsrd pdgnkidlvc damravmesi nphkyclsil
841 tshvkktpe leivlqkvhe lqgnapsdpd avsaeealky llhlvdvnel ydhsldtydf
901 dlvlmvaeks qkdpkeylpf lntlkkmetn yqrftidkyl kryekaighl skcgpeyfpe
961 clnlikdknl ynealklysp ssqqyqdisi aygehlmqeh myepaglmfa rcgahekals
1021 afltcgnwkq alcvaqlnf tkdqlvglgr tlagklveqr khidaamvle esaqdyeeav
1081 llllegaawe ealrlvykyn rldiietnvk psileaqkny mafldsqtat fsrhkkrllv
1141 vrelkeqaqq aglddevphg qesdlfsets svvsgsemssg kyshsnsris arssknrrka
1201 erkkhslkeg splldalle alsevvqnte nlkdevyhil kvlflfefde qgrelqkafe
1261 dtlqlmersl peiwtltyqq nsatpvlqpn stansimasy qqktsvpvl daelfippki
1321 nrqtgwklsl ld

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M_musculus	1	MRNLKLRHRTLEFRDIOAPK...OCFLRNE...QGTVLIG
H_sapiens	1	MRNLKLRHRTLEFRDIOCPNP...OCFLRNE...QGTVLIG
D_melanogaster	1	MRNLKLRHC...MNAVAHP...QHLLQPELGGSDIY
S_cerevisiae	1	MVEHDKSGSKRQELRSNMRNLITLNGKKEPTASTAEGEDDSTFLDDEVFITLDSIT
A_thaliana	1	MRNLKLESEPP...QITOLHSTEVVQFAAEDDQSRLEFSSAN
C_elegans	1	MRNLKLESEPP...MKNLQSGSKTSENPEIAGADDFH
M_musculus	37	SERGLTEVDP...VREVKTEISLVAEGFLPEDGSGCIVGIDLLDQESVCVATASGDVIV
H_sapiens	37	SEHGLTEVDP...VSREVKNEISLVAEGFLPEDGSGRIVGVQDILLDQESVCVATASGDVIV
D_melanogaster	36	FVYADNKIYA...VOESGDVRLKVIAR...LPT...IVGVFELQDNLKCVAS...GCVIT
S_cerevisiae	61	CVLGSTLGLGIEVQOFMKDGSRLVLAENIOTFDN...SFFVHFADINQVVFVFEQGDIT
A_thaliana	43	FVYALQLSSFQNESAGAKSAMPVEVCSIDIEPGD...FITTFDYLAKKESLGLTEGLLV
C_elegans	27	PELQTIASVSKNELLLHNNLISSTIKWAEQRRELE...SISERTDGNQEVVILADGRA
M_musculus	95	C...NLSTOOLECVGSVASGISVMSWSPDQELL...LATQOTLIMMTKDFEVIARQ
H_sapiens	95	C...SLSTOOLECVGSVASGISVMSWSPDQELL...LATQOTLIMMTKDFEPIEQO
D_melanogaster	87	V...LPOTGATSEGTFCVCIEMMNSPNOENAEVTRTHNIMMTSTFVIAEQP
S_cerevisiae	121	ATYDPSLDP...KETLEITMG...NCIAAQS...VDEETLAVTKDRN...SKLPEPISBYH
A_thaliana	102	...HNVSDVTEHVGNLCCGKICSPNETGDLGLITGLGQ...VITDWMALMYKA
C_elegans	87	VEDGEVMD...LEIAELTATVSAAE...ADEGTLALADN...QTVIADSSLVFEARER
M_musculus	148	T...HODDFGEGKFFVTVGWGSKTOFHGSEGRPAFPV...OLPENALPWWDD
H_sapiens	148	T...HODDFGESKFFVTVGWGSKTOFHGSEGRQAAFOM...OMHSEALPWWDD
D_melanogaster	140	T...DAELDP...QCVNVGWGCKKTOFHGSEGRQAARK...ESDSFPRDQOE
S_cerevisiae	181	L...EVDLKI...SKHVTVGWGSKTOFHGSGKARAME...ASL...ASGLVGNQ...RDP...YMVD
A_thaliana	155	L...GEVPEGGYV...RET...
C_elegans	140	LIFSNERKKSAPVNVGWGSESTOFHGSAGKLPGEKIEKEK...
M_musculus	195	R...SH...LWRGDCGFYAVSVV...CROTEARKIRVKNRE...FALQSTS
H_sapiens	195	R...SQ...LWRGDCGFYAVSVV...CPETGARKREVKNRE...FALQSTS
D_melanogaster	187	L...NOFVSIISWRGDGEFVSVV...AAALG...RTFVYDSE...GRLNHTA
S_cerevisiae	240	TGCVT...SHH...ISWRGDCGFYAVSVV...EVEDDETSIKRRAFVFSRE...GOLDSAS
A_thaliana	168	...NDH...CGGISISWRGDGKFAT...MGEVYSGCM...SKK...WSES...GALOSIS
C_elegans	181	...KOEQHSKTSVHRWGDGFYAVSF...YSS...NDIRN...TVDRNGEIT...NMNM
M_musculus	235	GSVPCGLPALAWKPSGSLIASTQDK...PNQODIVFEKNGLLHGHFTLPFLKDEVK
H_sapiens	235	EPVAGLGPALAWKPSGSLIASTQDK...PNQODIVFEKNGLLHGHFTLPFLKDEVK
D_melanogaster	229	EKSANLKD...VVRP...GNWIAVPOOF...PNKSTIALFEKNGLRHRELVLPPFDQEEP
S_cerevisiae	299	EPVVG...HQLS...WKPSGSLIASTQDK...EHSVD...FEKNGLRHRELVLPPFDQEEP
A_thaliana	219	ETKEFTQ...ILEW...PSCAKIAAVYKK...SDOSSPSIAFEKNGLRHRELVLPPFDQEEP
C_elegans	230	IRNIYLSHCFAHKNANLCS...QENGSD...RIVT...EENGETNSVYKWD...EDED
M_musculus	289	...VNDLLWNADSSVLAWLEDLFEDSS...LKSYVOLWTVGNHYHWYKQSLFSTGKNO
H_sapiens	289	...VNDLLWNADSSVLAWLEDLFEDSS...LKSYVOLWTVGNHYHWYKQSLFSTGKSK
D_melanogaster	283	...VVOLRWSEDSDELAI...RTCAKEEQR...VYL...TEGNHYHWYKQSLFSTGKNO
S_cerevisiae	357	...VESVCNSNSSEALAY...V...ANRTOLWTSKNYHWYKQSLFSTGKNO
A_thaliana	277	...CENLKNNSASDILA...GVVSCPTYDA...TRV...FSSNNHYHWYKQSLFSTGKNO
C_elegans	286	RRITEKTEWNSGTGLSL...QTSLGK...HOLF...HHSNVEFTRKCYWFESE...
M_musculus	346	IVSLHWDE...VTPCRLHVLCTGWRYLCCDWHHTTDRSSGNSANDL...NVAVIDGNRVLTV
H_sapiens	346	IVSLHWDE...VTPCRLHVLCTGWRYLCCDWHHTTDRSVGNSNDL...NVAVIDGNRVLTV
D_melanogaster	331	HALLHWDRRCGHEHTLHVLKESGKHLVYRGAFAVDNN...SIVEVIDGKRLITD
S_cerevisiae	398	ISYK...HFE...KDETFMFSDA...FINIV...DFAYKMAQGPTLEPFNGTSLVMDGRVMTPT
A_thaliana	325	...VYVWDE...TKELQHCWTLSCGVSVRHFMTVT...AVVEDSTAFVIDNS...SLVTP
C_elegans	334	...SLKRWSTVECONEVVLESQGFVSVH...IPTASFSDV...SONV...VATD...EGRYS
M_musculus	404	FRQTVVPPPMCTYRLIPHPVNOVIFS...AH...IGNDLAVLDASNOISVYKCG...DMPN
H_sapiens	404	FRQTVVPPPMCTYRLIPHPVNOVIFL...AHPQKSNDLAVLDASNOISVYKCG...DCPS
D_melanogaster	384	EDENIVPPPMKSKE...LOKPE...MLMPDA...PSSGLHLA...RLTH
S_cerevisiae	455	LAL...NVPPPMYIRDFETEGNVLDVACSFSEIYAAINKDVLFAAVPSHEEMKKG...KEPS
A_thaliana	376	LSL...VPPPMYLSLSSESSAARDAYYRNS...KNC...AVFL...DGLISFV...EPFA
C_elegans	387	LCRRVPPPMCDYSLQCLSD...VAV...TSTHHVHVITSDWK...SCHLFFKKKRNYSNPF
M_musculus	457	MDSTVKLGAVGGNGFKVPLATPHLEKRYSTOFGNNE...EEDAL...LSL...LTWVE...DTFLA
H_sapiens	459	ADPTVKLGAVGGSGFKVCLRTPHLEKRYKIOENNE...DQVN...FLKGLLTWVE...EEDFLA
D_melanogaster	420	ESPHYL...ATHSSAG...STRLLLSYK...DNDNKPG...W...EYR
S_cerevisiae	514	IVCE...PKSEFTSEVSLROMABINDSIVGVLLD...DNL...SRKLL...IDQIT...
A_thaliana	427	PNTWED...EGKDFSEISDCKTALGSFVHL...WLVHSLLCVAYGSSHNK...CLSSGGYDTE
C_elegans	445	ERKKYI...EILKVP...SH...TYFACFAMSQD...TDGYKFN...SDRAS...EDV...HTEVTEG...ICG

FIG. 1. Comparison of the amino acid sequence of Ikap across several species. Alignment of the amino acid sequence of Ikap (*M\_musculus*) with that of *Homo sapiens* (*H\_sapiens*), *Drosophila melanogaster* (*D\_melanogaster*), *Saccharomyces cerevisiae* (*S\_cerevisiae*), *Arabidopsis thaliana* (*A\_thaliana*), and *Caenorhabditis elegans* (*C\_elegans*). Black boxes indicate identical AA, while conserved AA residues are shown in gray. Asterisk (\*) at AA position 696 for mouse and human proteins indicates the location of the heterozygous R696P mutation found in only 4 FD patients. Sequence alignments were made using Pileup and Boxshade commands from GCG Wisconsin Package V.9.0 (Madison, WI).

Figure 9

M_musculus	517	SYSHSSSSQSIHHLTVHSEVDEEQQGLVSSSVTVDGVVIGLCCC.SKTRKSLAVOLAD
H_sapiens	517	VSHSESPRSVIHHLTAASSEDEEHGOLVSSSVTVDGVVIGLCCN.SKTRKSEVLOLAD
D_melanogaster	456	V.HSSVRINGVNAVAHYALNEFYVO.TVNNNGHTY...SL...KADKRLKVERSY
S_cerevisiae	562	TOPLLNIVEVYD.VILRSFDYNHLVYE...TRDGTVCOLD...AF
A_thaliana	486	EHGSIYOEVEVYCHEDHVEDVTCSGFKASIFQQLFSPVHALAWNPSKRDSAFVFEFEG
C_elegans	500	FVYDEPSESYSILWNYSKHKHS...REGANPEKIFEGENICWIGVNPSNKHPEASND
M_musculus	576	GOVLKILWESPSLAIPWKNSSEGIPIVRFVHPCTOMEVANIGGEECVLGLTDRCRFFILVT
H_sapiens	576	GOFFKYLWESPSLAIPWKNSGGFVRFVHPCTOTETAMICEECVLGLTDRCRFEIND
D_melanogaster	507	VOI...HEPADQID.VVIVKG...CIWD...GYTGANTLRCHLLEIGY
S_cerevisiae	604	GOMNETT.KEPOL.VRDFVVKR...VNTSAEDDDNWAESESLVAFGCTINGCLEANOV
A_thaliana	546	GKVLGYASRSEIMETRSSDSEVCFPSTCQWVRVAQVDAAGVHKPLCGLDPMGRLSINGK
C_elegans	556	CKFTEDINTKEELFKIDKFESNEVHFQVCHGILNHHVIOV...DNSMLEPSE
M_musculus	636	EVASNITSFA.....VCDFELLTTHSH....TCQCFSSGASLKMLOAALSSSHEA
H_sapiens	636	EVASNITSFA.....VYDFELLTTHSH....TCQCFCLRDASFRTLOAGSSSNHVS
D_melanogaster	548	REGEETTSFC.....VVTLLVYTO.....LNAHFEVLD...DRROVA
S_cerevisiae	659	LASAMTSLE.....ETOSLELTTAACH....NLOFVHNSIDEKPLPLVEEG...V
A_thaliana	606	NECNCSSESYSELANE.VTBLTKQDFEINOTRDVLNGDVLGNVFFVVDGRNRD
C_elegans	606	RVSQPAISILTRG.....SDILLDEFDNLRFTDAE.....S
M_musculus	684	SGE...RKVVWVGSRIVTVV.PQDKILLOMPRGNLEV.HRALVLAQIRKWLDKLMEKE
H_sapiens	684	HGEV...RKVERGSRIVTVV.PQDKILLOMPRGNLEV.HRALVLAQIRKWLDKLMEKE
D_melanogaster	584	S.....RNTPERGSRIVTVV.ARKARVLOMPRGNLEHCPRLVLLELYGDLLEGG...OK
S_cerevisiae	704	EDER...VRALERGSIVSVT.PSKESVLOATRGNLETIYPRIVLALARKNMAKREKE
A_thaliana	666	EENNSYVNIWERGSGVIGVGDAAVILQTMGRNLECIYPRKLVLSITNALAQOREKE
C_elegans	638	GKTLDVRNVEAGCEV.ACHSOSANVILQARGNLETIOPRYVVAHTRDLDLDEKEMIA
M_musculus	741	AFECMRKLRINLNLIHD.HNPKVFLNENVETFFVFOIDSUNHINLFFTELNEEDVTKTMYPP
H_sapiens	741	AFECMRKLRINLNLIHD.HNPKVFLGNVETFFKQIDSUNHINLFFTELKEEDVTKTMYPA
D_melanogaster	637	AFEMSRKQRINLNLIHD.HQVKRFVSSVGFINDINEPFWCLELHQLONEDFTKGMYS
S_cerevisiae	761	ABIVCRTHRINLIHD.YAPEVFLNENVETFFVFOIDSUNHINLFFTELNEEDVTKTMYKE
A_thaliana	726	APNLRRHRIDFNLIHDVLYGWAQFLOSAVFVEOVNENHYTEVCAKKNEDVTEFYKK
C_elegans	797	SEKWMKRRHVMDS.....SAMKYKGDDEDD...P
M_musculus	800	.....PITK.SVOYST...HPDGKKHDLCDAMRAAM..EAINPRKECLS
H_sapiens	800	.....PWS.SVYLS...DPDGNKLDVCDAMRAVM..EAINPRKECLS
D_melanogaster	696	NY.....DANK.STYPSD...YRVDQKVYVCRLEQQM...NRF.VSERLP
S_cerevisiae	820	TLVSGISKSFGMEPAPIEMOYKKNFDPKISKVKECDALNVLSNPEYKKKLOL
A_thaliana	786	FSISKKGDEVF.....EVRKSCSNKVSSVLOAKRAKEEHIPESPSRELC
C_elegans	725	IWLKTSNDSQFEQLLICTEVE...EDAGSSLCMTVARYED...LSDAEKTNPPI
M_musculus	839	ILTSHVKKTTPELE...IVLQKVQELQGNLPFDP...ESVSVEEALKYLLLVVDVNELE
H_sapiens	839	ILTSHVKKTTPELE...IVLQKVHLEQGNAPSDP...DVSAAEALKYLLHLVDVNELE
D_melanogaster	736	ETAYVVLGC...LE...MALQVWKEQ...QE...DASLADLLOHLLLVVDVNELE
S_cerevisiae	880	ETAYASQNPONLS...AALKLSELE...NSEEKDCSVTYLCLFQDVNVV
A_thaliana	831	ILTLANSDPPATEMLREKSKVREMLLNSDDIRKSCPSAEEALKHLLWLDSEAIF
C_elegans	777	ILTALLSKPSKYNDC...LKEVQE...HVEKTIADSKDVFRNSLHHSFFVPAKELF
M_musculus	892	NHSLGTYDFNLVLMVAEKSQKDPKEYLPFLNLTLLK.METNYOREFTIDKYLKRYEKAIGHL
H_sapiens	892	DHSLGTYDFNLVLMVAEKSQKDPKEYLPFLNLTLLK.METNYOREFTIDKYLKRYEKAIGHL
D_melanogaster	782	NVALGTYDFGLVLFVAKSQKDPKEYLPFLNLTLLK.EPIDYRFRIDDLKRYTSALSHL
S_cerevisiae	926	KSALSLYDVSLALVAKSQKDPKEYLPFLNLTLLK.NEPLRREPIDDYLGNYEKAIDHL
A_thaliana	891	EALGLYDLNLAAVVALNSQKDPKEYLPFLNLTLLK.MPESLMEKIDIKLQRTSALRNT
C_elegans	829	NCAISTYDLKLAQQAASNYDPKEYLVNKLNRVMTLEEQRTINVVREAWIDAVSSL
M_musculus	951	.....SKCGPE..YFTECLNLIKDK.NLYKEALKLYRPSPOVQAASMAVGEHLMQEHM
H_sapiens	951	.....SKCGPE..YFTECLNLIKDK.NLYNEALKLYSPSSQOYDISIAYGEHLMQEHM
D_melanogaster	841	.....KACGED..HMEALLEYIKKH.GLYTEGLAFYREHIFQKNLYVAYAHLEATAK
S_cerevisiae	985	.....SEIDKGNVSEEVYVYNESE.DLYRHGLALRYDSEKONVIYNIYAKHSSNOM
A_thaliana	950	.....VSAG..VGYPEDCNLIKKNPLPLCLLLIT.DPERKLVVLEAWADHLADEHR
C_elegans	889	FLLDSSKERGSEETWNNNIEELIQ.REKLYQALTLVKEGDRRYKQCCELYAABERKVR
M_musculus	1002	YEPAGLVARCGAQEKALAEFLACGSWOALCVAAQLOMSKDVAGLARTLAGKLVEORK
H_sapiens	1002	YEPAGLIMARCGAHERKALSFLACGNWQALCVAAQLOMFTKQDQGLERTLAGKLVEORK
D_melanogaster	892	LDNAELMYERGGOALQALLAKHTLDQORVLVHAKKLSEPLDOV...AQSLVGPLOQGG
S_cerevisiae	1038	YDAAYAVEMLGKLEKANGAKQAKRREAMSAAVO.KEP.EEVESYAEELISSITFAG
A_thaliana	1001	WEDAATTYLCCCKLEKASKARECCGDSGLRVGALRLGKDEKRLAYELCEEANLGG
C_elegans	948	WREAAFLVELSGNSEKTLKCHWMSRDVDGLAASARRAVDAGKKIKHAIKNTTFRBAQ

Figure 9

Continued

M\_musculus 1062 HSEAAVLECYAODYEEAVLLLEGSAAWEEALRLVYKYDRVLIETSEKPSILEAQKNYM  
H\_sapiens 1062 HETAAVLEESAODYEEAVLLLEGSAAWEEALRLVYKYDRVLIETSNVKPSILEAQKNYM  
D\_melanogaster 949 HSEAYEYKKEHCODRKROFDLLECHLYSRAYEAGLED..DDSEKAPAYGVVLE  
S\_cerevisiae 1096 YDEAADQLEYLDNVKEAVLYCKYRYEIASLVAIRAKKDEEEVVDPGGEFGILIA  
A\_thaliana 1061 PAEAAKTALEYCSDISGFTSLNREWEEALRYAHLTADDRIS.VVKSSALECASGLY  
C\_elegans 1008 PKELAKALKLAGSSSTWIVHPLCEFEWLPASREVEVGK....EEAKKKALSREDDY

M\_musculus 1122 DFLDSETATFERHKNRLQVVRALRRQAPQVHYDHEVAHGCPESDLF.SETSSIMS.GSEMS  
H\_sapiens 1122 AFLDSOTATFSEHKRLLVURELKEQAQAGDDDEVPHGOESDLF.SETSSIMS.GSEMS  
D\_melanogaster 1007 SSLQNLQLFDYKQRLLDLRNQAKEGEEEDTIV.NLKEVDLL.SDTSSHS..SEYS  
S\_cerevisiae 1156 ELADCKGQINSQLRRLREIRAKKEENPVAYGGEETEQAQDVSHAPSETSTQESFFRYT  
A\_thaliana 1120 SEFKESIEKVGKYLTRYLAVRERALLAALKSEERSVVDLDDTASEASSNMSGMSAYA  
C\_elegans 1063 MDERRKKEFENYKKRLAVVRENKLRVEQFAAGEV.....DILRDDISVHSISSR..

M\_musculus 1180 .GYSHSNR.ISARSSKNRR..KAERKKHSLKEGSPLEGLALLEAL....SEVVO.SVE  
H\_sapiens 1180 .GYSHSNR.ISARSSKNRR..KAERKKHSLKEGSPLEDLALLEAL....SEVVO.YTE  
D\_melanogaster 1063 .GTSRRGK...FRSSKNRR..KBERKLFSLKPGNPLEDALHNVKKAQ..LOE  
S\_cerevisiae 1216 .GNTGGKKTGASRTAKNR..EERKKARGKCKIYEE...EYLVQSVGKEE.RLN  
A\_thaliana 1180 LCTRRGSAISVSSNARSARDLRORKSGKTRAGSAGEEMALVHL....KGR.MTD  
C\_elegans 1115 .....SGSSKYSMASIVRRK.QIEKKKSLKEGGEYEDSALLNVLSENYRWENIGSE

M\_musculus 1231 KLKDEVNAILKVLFLEFEFEQAKELORAFESTLQLMERAVPEIWTPEAGQOSS..TTPVLG  
H\_sapiens 1231 NLKDEVYHILKVLFLEFEDEQKELOKAFESTLQLMERSPEIWTLYQONS..TTPVLG  
D\_melanogaster 1116 PMEDTCKAPLOANAAADPLAAALOREFKTLLOAYDAAGDEIWTPELRGNGLAHTTC  
S\_cerevisiae 1268 QTPDAVRVVEGTCRRNMREQARSTOKNEVYVLDLHKANVKIYSISEKDRERVEN..G  
A\_thaliana 1234 GGRREIKSLICIVTLGEMESACKLOOTABN.FQYSTVAAVEI.AHDTVSSSESVDEEVC  
C\_elegans 1168 FCFPWNFNII-----

M\_musculus 1289 PSSTANSIMASYQQQKTCVPALDAGVMPPKMDPRQWKLSLL  
H\_sapiens 1289 PNSTANSIMASYQQQKTSVPVLDAGFFIPPKINRRQWKLSLL  
D\_melanogaster 1176 PN..VDYALQKEORYALISPLKR..FKPOL..MMDWQHEHLLQ  
S\_cerevisiae 1326 EVYYIPEIPVPEIHDFFPKSHVDF-----  
A\_thaliana 1292 FERYQKTRSTARDSDFSWMRK..VFIS-----  
C\_elegans 1178 -----

Figure 9  
Continued

100441856-010702

TABLE 2. COMPARISON OF THE NOVEL MOUSE *Ikbkap* GENE WITH MULTIPLE SPECIES HOMOLOGS

Species	Gene name	No. of amino acids	Molecular weight (kDa)	% aa identity with M.m.	GenBank Accession No.
<i>Mus musculus</i> (M.m.)	<i>Ikbkap</i>	1332	149.11	—	AF367244
<i>Homo sapiens</i>	<i>IKBKAP</i>	1332	149.11	80	AF153419
<i>Drosophila melanogaster</i>	<i>CG10535</i>	1213	138.21	32	AAF54670
<i>Saccharomyces cerevisiae</i>	<i>Elp1/Iki3p</i>	1349	152.99	29	AAB67278
<i>Arabidopsis thaliana</i>	Unknown	1308	146.63	27	BAB08695
<i>Caenorhabditis elegans</i>	Unknown	1177	134.80	24	AAF60430

Figure 10

10041856 010702

TABLE 1. MOUSE *Ikkap* EXON AND INTRON BOUNDARIES

Exon	Acceptor site	Donor site	Size (bp)	cDNA position
1		AGgtgagcattcgccc	129	1..129 <sup>a</sup>
2	ttttttccctcagAA	AAgtaggtcactgatgc	163	130..292 <sup>b</sup>
3	tatgctttgtgaagGT	AGgtaggtgtaaggcct	153	293..445
4	ttttctctgatgcagCT	AGgtaagctttgcactg*	82	446..527
5	acatgaactcctaagCT	AGgtaagcggttcttgg	81	528..608
6	cttgaaaaactgtagGC	TGgtaaggcgggatgat	86	609..694
7	gggtctctcttcagCC	TGgtgtctctcttcagc*	97	695..791
8	ctacctcctttgcagAG	AAgtgagtgcataaaa*	91	792..882
9	aggttctgctttcagAC	AGgtaggggtcagagtt	124	883..1006
10	tttgtccctaccagGT	TGgtatgacagcttg	94	1007..1100
11	tcctccacacacagTC	AAgtaagttgctgcgaa	231	1101..1331
12	cttttcattgtgtagAC	TGgtaagtggaagcagg	165	1332..1496
13	tttttgtttctagGT	TCgtaagttcctaata	100	1497..1596
14	ctaataattgaacagGA	AGgtatcatggttcatc	189	1597..1785
15	ttttttgcttttagTT	GGgtgaggatcagagtt	107	1786..1892
16	ttaatcttacaacagAG	AGgtgaatagacacggc	104	1893..1996
17	ttcatttcttgcagGA	AGgtatgtaggcttgg	54	1997..2050
18	tcttgcctgttgcagGT	AAgtaagctctcctata	106	2051..2156
19	cactgggtatttttagTG	AGgtaagctgactcttc*	116	2157..2272
20	gggtttatttttagAT	AAgtaagttatttct*	74	2273..2346
21	ttcctgtcctcacagAC	AGgtacactttgcgtct	79	2347..2425
22	tactttctttgatagGT	AGgtaagttatttgata*	80	2426..2505
23	tactgtgggttcttagGG	AAgtgggtgctgtgtgt	138	2506..2643
24	cacttactacctcagGT	AGgtagagacctgcgcg*	86	2644..2729
25	cttaaaactccaacagGA	AGgtatgtggagttgag*	149	2730..2878
26	aactttttcttaggGA	TGgtaagggtttttt	124	2879..3002
27	ttttttttttcagGA	AGgtatgtgggtgggtta*	98	3003..3100
28	cgtctcttgcacagGC	AGgtaagcagggccatt	202	3101..3302
29	ttgctgtctttcagGA	AGgtgagctcctcccc	62	3303..3364
30	ctcttccctgtcagGA	TGgtaaggagctctga	63	3365..3427
31	ttcttccctcttagGT	AGgtgaggattacattt*	61	3428..3488
32	attatgcacctcagCC	GGgtgagtgccctccaaa*	114	3489..3602
33	gttcattctctctagAT	GCgtacgtacgagacct*	112	3603..3714
34	tgttaattctgacagGA	AGgtatggcttcagtgc	128	3715..3842
35	ccatttctctctagAT	CGgtaagcttccctcaga	155	3843..3997
36	ctgttttctgcttagGT	CGgtgtactgtctgttc	76	3998..4073
37	cattcttgcttccagAT		709	4074..4799 <sup>c</sup>

Figure 11

10041855.010702

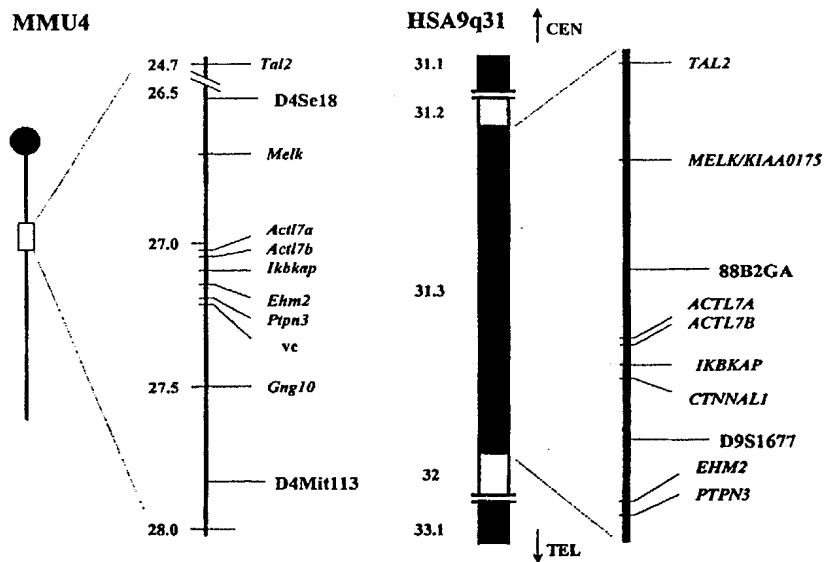


Figure 12